APPENDIX A:
BLAST SEARCHES

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tigr db
arabidopsis thaliana

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Arabidopsis thaliana Blast Search

BLASTN 2.0MP-WashU [10-May-2005] [linux26-i686-ILP32F64 2005-05-10T21:11:22]

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Reference: Gish, W. (1996-2005) http://blast.wustl.edu

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak protein similarities
encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= query_sequence NGGGGAGGATN or NGCGGAGGCTN
            (11 letters)

WARNING: the maximum achievable score of 55 for gapped alignments in frame +1
          is less than the gapped cutoff score gapS2 (=81).

WARNING: the maximum achievable score of 55 for gapped alignments in frame -1
          is less than the gapped cutoff score gapS2 (=81).

Database: ATH1.cdna
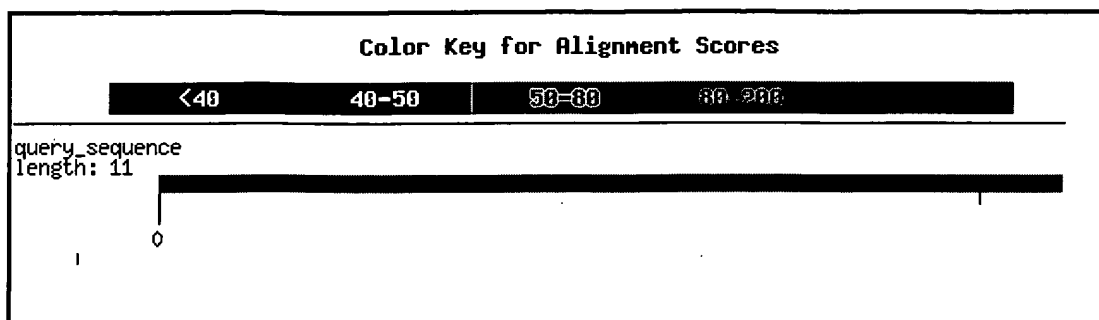   28,952 sequences; 43,903,363 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

	High	Smallest Sum Probability	
Sequences producing High-scoring Segment Pairs:	Score	P(N)	N

          *** NONE ***

Distribution of Blast Hits on the Query Sequence

| Mouse-over to show name and scores. Click to show alignments. |

```
                          Color Key for Alignment Scores
          ┌───────────┬───────────┬───────────┬───────────────────┐
          │    <40    │   40-50   │   50-80   │      80-200        │
          └───────────┴───────────┴───────────┴───────────────────┘

query_sequence
length: 11

           ████████████████████████████████████████████████████████████
           |                                                         |
           0
     I
```

Parameters:
  filter=dust
  E=10
  B=20
  V=20
  cpus=1
  -o blastn-annotation_dbs_ATH1.cdna-15763-1155058214

  ctxfactor=2.00

Query Strand	MatID	Matrix name	----- As Used ----- Lambda	K	H	----- Computed ---- Lambda	K	H
+1	0	+5,-4	0.192	0.182	0.357	same	same	same
		Q=10,R=10	0.104	0.0151	0.0600	n/a	n/a	n/a
-1	0	+5,-4	0.192	0.182	0.357	same	same	same
		Q=10,R=10	0.104	0.0151	0.0600	n/a	n/a	n/a

Query Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+1	0	11	11	9.6	134	11	n/a	73	0.048	51
								134	0.046	81
-1	0	11	11	9.6	134	11	n/a	73	0.048	51
								134	0.046	81

Statistics:

  Database: /usr/local/db/euk/pub/a_thaliana/annotation_dbs/ATH1.cdna
    Title: ATH1.cdna
    Posted: 12:55:19 PM EST Feb 9, 2004
    Created: 11:06:03 AM EST Feb 9, 2004
    Format: XDF-1
    # of letters in database: 43,903,363
    # of sequences in database: 28,952
    # of database sequences satisfying E: 0
  No. of states in DFA: 8 (8 KB)
  Total size of DFA: 9 KB (2050 KB)
  Time to generate neighborhood: 0.00u 0.00s 0.00t Elapsed: 00:00:00
  No. of threads or processors used: 1
  Search cpu time: 0.02u 0.01s 0.03t Elapsed: 00:00:00
  Total cpu time: 0.02u 0.01s 0.03t Elapsed: 00:00:00
  Start: Tue Aug 8 13:30:14 2006   End: Tue Aug 8 13:30:14 2006
WARNINGS ISSUED: 2

Please report problems to blast@tigr.org